IN THE CLAIMS

Claims 1-11 (Cancelled)

Claim 12 (Withdrawn): A process for the fermentative preparation of an L-amino acid, comprising:

a) fermenting coryneform bacteria which produce the L-amino acid and in which at least the *rpsL* gene or nucleotide sequences which code for it are enhanced,

b) concentrating the L-amino acid in the medium or in the cells of the bacteria, and

c) isolating the L-amino acid.

Claim 13 (Withdrawn): A process as claimed in claim 12, in which at least the *rpsL* gene or nucleotide sequences which code for it are over-expressed.

Claim 14 (Withdrawn): A process as claimed in claim 12, wherein the L-amino acid is L-lysine.

Claim 15 (Withdrawn): A process as claimed in claim 12, wherein bacteria in which further genes of the biosynthesis pathway of the desired L-amino acid are additionally enhanced are employed.

Claim 16 (Withdrawn): A process as claimed in claim 12, wherein bacteria in which the metabolic pathways which reduce the formation of the L-amino acid are at least partly eliminated are employed.

Claim 17 (Withdrawn): A process as claimed in claim 12, wherein the bacteria are transformed with a plasmid vector, wherein the plasmid vector carries the nucleotide sequence which codes for the *rpsL* gene.

Claim 18 (Withdrawn): A process as claimed in claim 12, wherein the expression of the polynucleotide(s) which code(s) for the *rpsL* gene is enhanced.

Claim 19 (Withdrawn): A process as claimed in claim 12, wherein the expression of the polynucleotide(s) which code(s) for the *rpsL* gene is over-expressed.

Claim 20 (Withdrawn): A process as claimed in claim 12, wherein the regulatory/catalytic properties of the polypeptide for which the polynucleotide *rpsL* codes are increased.

Claim 21 (Withdrawn): A process as claimed in claim 12, wherein in the bacteria one or more of the genes selected from the group consisting of

the dapA gene which codes for dihydrodipicolinate synthase,

the gap gene which codes for glyceraldehyde 3-phosphate dehydrogenase,

the tpi gene which codes for triose phosphate isomerase,

the pgk gene which codes for 3-phosphoglycerate kinase,

the zwf gene which codes for glucose 6-phosphate dehydrogenase,

the pyc gene which codes for pyruvate carboxylase,

the mqo gene which codes for malate-quinone oxidoreductase,

the lysC gene which codes for a feed-back resistant aspartate kinase,

the lysE gene which codes for the lysine export protein,

the zwa1 gene which codes for the Zwa1 protein, and

the rpoB gene which codes for RNA polymerase B,

is or are enhanced or over-expressed.

Claim 22 (Withdrawn): A process as claimed in claim 12, wherein in the bacteria one or more of the genes selected from the group consisting of

the pck gene which codes for phosphoenol pyruvate carboxykinase,

the pgi gene which codes for glucose 6-phosphate isomerase,

the poxB gene which codes for pyruvate oxidase,

the zwa2 gene which codes for the Zwa2 protein

is or are attenuated.

Claim 23 (Withdrawn): A process as claimed in claim 12, wherein the bacteria are *Corynebacterium glutamicum.*

Claim 24 (Cancelled)

Claim 25 (Withdrawn): A process for discovering RNA, cDNA and DNA in order to isolate nucleic acids or polynucleotides or genes which code for the ribosomal protein S12 or have a high similarity with the sequence of the *rpsL* gene, which comprises employing the polynucleotide comprising the polynucleotide sequences as claimed in claim 89 as a hybridization probe.

Claim 26 (Withdrawn): A process as claimed in claim 25, which is conducted on an array, micro array, or DNA chip.

Claim 27 (Withdrawn): A process for identifying a nucleic acid which codes the ribosomal protein S12 or a high similarity with the sequence of the *rpsL* gene, comprising:

contacting a sample with the polynucleotide sequence as claimed in claim 89 under hybridization conditions such that the polynucleotide sequence as claimed in claim 89 hybridizes with said nucleic acid when said nucleic acid is present in the sample.

Claim 28 (Withdrawn): The process of claim 27, wherein said nucleic acid is present in the sample.

Claim 29 (Withdrawn): The process of claim 28, further comprising isolating said nucleic acid.

Claim 30 (Withdrawn): The process of claim 27, wherein said nucleic acid is not present in the sample.

Claims 31-40 (Cancelled)

Claim 41 (Currently Amended): An isolated polynucleotide comprising a polynucleotide sequence selected from the group consisting of:

a) a polynucleotide which is at least 95% identical to a polynucleotide which encodes SEQ ID NO: 4 and which encodes a polypeptide which increases lysine production in corynebacteria, and

b) a polynucleotide which encodes a polypeptide which is at least 95% identical to SEQ ID NO: 4 and which encodes a polypeptide which increases lysine production in corynebacteria,

wherein said polypeptide of a) or b) comprises an arginine residue at the position corresponding to position 43 in SEQ ID NO: 4.

Claim 42 (Previously Presented): The polynucleotide of Claim 41, which is at least 95% identical to a polynucleotide which encodes SEQ ID NO: 4 and which encodes a polypeptide which increases lysine production in corynebacteria.

Claim 43 (Previously Presented): The polynucleotide of Claim 41, which is at least 97% identical to a polynucleotide which encodes SEQ ID NO: 4.

Claim 44 (Previously Presented): The polynucleotide of Claim 41, which is at least 95% identical to SEQ ID NO: 3.

Claim 45 (Previously Presented): The polynucleotide of Claim 41, which is at least 97% identical to SEQ ID NO: 3.

Claim 46 (Currently Amended): An isolated polynucleotide which hybridizes to SEQ ID NO: 3 under stringent conditions and which encodes a polypeptide which encodes a polypeptide which increases lysine production in corynebacteria,

wherein stringent conditions comprise hybridization in 5x SSC and washing in 2x SSC at a temperature ranging from 50°C to 68°C,

wherein said polypeptide of a) or b) comprises an arginine residue at the position corresponding to position 43 in SEQ ID NO: 4.

Claim 47 (Previously Presented): The polynucleotide of Claim 46, which comprises SEQ ID NO: 3.

Claim 48 (Previously Presented): The polynucleotide of Claim 41, which is RNA.

Claim 49 (Previously Presented): The polynucleotide of Claim 41, which comprises SEQ ID NO: 3, or a fragment of SEQ ID NO: 3 comprising residue 43, which encodes a polypeptide which increases lysine production in corynebacteria.

Claim 50 (Previously Presented): The polynucleotide of Claim 41, which consists of SEQ ID NO: 3.

Claim 51 (Previously Presented): The polynucleotide of Claim 41, which encodes a polypeptide which is at least 95% identical to SEQ ID NO: 4.

Claim 52 (Previously Presented): The polynucleotide of Claim 41, which encodes a polypeptide which is at least 97% identical to SEQ ID NO: 4.

Claim 53 (Previously Presented): The polynucleotide of Claim 41, which encodes a polypeptide which is at least 99% identical to SEQ ID NO: 4.

Claim 54 (Previously Presented): The polynucleotide of Claim 41, which encodes the polypeptide of SEQ ID NO: 4.

Claim 55 (Previously Presented): The isolated polynucleotide of Claim 41, which encodes a polypeptide at least 95% identical to SEQ ID NO: 4 and that has at least one amino acid substitution between positions 38-48 of SEQ ID NO: 4, wherein expression of said polypeptide in a coryneform bacterium increases the production of lysine compared to expression of the polypeptide of SEQ ID NO: 2.

Claim 56-58 (Cancelled)

Claim 59 (Previously Presented): A vector comprising the isolated polynucleotide of Claim 41.

Claim 60 (Previously Presented): A vector comprising the isolated polynucleotide of Claim 46.

Claim 61 (Previously Presented): A vector comprising the isolated polynucleotide of Claim 55.

Claim 62 (Previously Presented): A host cell comprising the isolated polynucleotide of Claim 41.

Claim 63 (Previously Presented): The host cell of Claim 62, wherein said polynucleotide is present in multiple copies.

Claim 64 (Previously Presented): The host cell of Claim 62, further comprising a promoter, ribosome binding site, expression cassette or regulation region upstream from said polynucleotide.

Claim 65 (Previously Presented): The host cell of Claim 62, which is a coryneform bacterium.

Claim 66 (Previously Presented): The host cell of Claim 62, which is *Corynebacterium glutamicum*.

Claim 67 (Previously Presented): A host cell comprising the isolated polynucleotide of Claim 46.

Claim 68 (Previously Presented): The host cell of Claim 67, wherein said polynucleotide is present in multiple copies.

Claim 69 (Previously Presented): The host cell of Claim 67, further comprising a promoter, ribosome binding site, expression cassette or regulation region upstream from said polynucleotide.

Claim 70 (Previously Presented): The host cell of Claim 67, which is a coryneform bacterium.

Claim 71 (Previously Presented): The host cell of Claim 67, which is *Corynebacterium glutamicum*.

Claim 72 (Previously Presented): A host cell comprising the isolated polynucleotide of Claim 55.

Claim 73 (Previously Presented): The host cell of Claim 72, wherein said polynucleotide is present in multiple copies.

Claim 74 (Previously Presented): The host cell of Claim 72, further comprising a promoter, ribosome binding site, expression cassette or regulation region upstream from said polynucleotide.

Claim 75 (Previously Presented): The host cell of Claim 72, which is a coryneform bacterium.

Claim 76 (Previously Presented): The host cell of Claim 72, which is *Corynebacterium glutamicum*.

Claim 77 (Previously Presented): An isolated coryneform bacterium comprising the polynucleotide of Claim 56.

Claim 78 (Previously Presented): An isolated coryneform bacterium comprising the polynucleotide of Claim 57.

Claim 79 (Previously Presented): An isolated coryneform bacterium comprising the polynucleotide of Claim 58.

Claim 80 (Previously Presented): An isolated coryneform bacterium comprising the polynucleotide of Claim 50.

Claim 81 (Previously Presented): *Corynebacterium glutamicum* strain DM1545 deposited as DSM 13992 at the Deutsche Sammlung für Mikroorganismen und Zellkulturen (DSMZ, German Collection of Microorganisms and Cell Cultures, Braunschweig, Germany).

Claim 82 (Previously Presented): A process for preparing an amino acid comprising:

culturing the host cell of Claim 62 in a medium for a time and under conditions suitable for the fermentive production of said amino acid, and

recovering or isolating said amino acid.

Claim 83 (Previously Presented): The process of Claim 82, wherein said amino acid is L-lysine.

Claim 84 (Previously Presented): A process for preparing an amino acid comprising:

culturing the host cell of Claim 67 in a medium for a time and under conditions suitable for the fermentive production of said amino acid, and

recovering or isolating said amino acid.

Claim 85 (Previously Presented): The process of Claim 84, wherein said amino acid is L-lysine.

Claim 86 (Previously Presented): A process for preparing an amino acid comprising:

culturing the host cell of Claim 72 in a medium for a time and under conditions suitable for the fermentive production of said amino acid, and

recovering or isolating said amino acid.

Claim 87 (Previously Presented): The process of Claim 86, wherein said amino acid is L-lysine.

Claim 88 (Cancelled)

Claim 89 (Currently Amended): An isolated polynucleotide fragment of SEQ ID NO: 1 consisting of at least 15 consecutive nucleotides of nucleotides 1-499 or 884-1775 of SEQ ID NO: 1, or the full complement thereof.

Claim 90 (Currently Amended): An isolated polynucleotide fragment of SEQ ID NO: 1 comprising at least 20 consecutive nucleotides of SEQ ID NO: 1, or the full complement thereof.

Claim 91 (Currently Amended): An isolated polynucleotide fragment of SEQ ID NO: 1 comprising at least 30 consecutive nucleotides of SEQ ID NO: 1, or the full complement thereof.